line 30, delete "additional preparatory techniques" and substitute ---some special procedure---;

Page 24, line 19, after the word "and" insert ---the--;

Page 36, line 29, after "5%" insert a period ---.---;

Page 41, line 24, delete "Lumonics" and substitute ---LUMONICS---; and

Page 46, line 29, after "method" insert a period ---.---.

In the claims:

Kindly cancel claims 1-30 as originally filed and cancel any and all subsequently added claims added by amendment therein and substitute the following claims 31-47 therefor:

---31. A method for quantifying an analyte disposed in a specimen, said method comprising the steps of:

a) ensuring that said specimen contains an internal reference species (IRS) in a known concentration to calibrate all subsequent steps; whereby said specimen, upon being ensured that it contains an IRS, is referred to as an IRS-containing specimen;

b) capturing and isolating said analyte and said IRS, wherein said capturing and isolating step comprises a substep of combining said IRS-containing specimen with an affinity reagent;

c) quantifying said analyte in which said quantifying step comprises using mass spectrometric analysis to resolve distinct signals for said analyte and said IRS to determine the ratio of the analyte signal to the IRS signal.---;

---32. A method according to claim 31, in which said quantifying step further comprises using standard addition analysis.---;

---33. A method according to claim 31, in which said quantifying step further comprises using working curve analysis.---;

---34. A method according to claim 31, in which said quantifying step further comprises using working curve analysis calibrated only at a single point.---;

---35. A method according to claim 31, in which said quantifying step further comprises using multiple internal reference species at varying concentrations to display a working curve directly in a single mass spectrum which also contains the analyte signal.---;

---36. A method according to claim 32, in which said standard addition analysis comprises substeps of first, dividing said IRS-containing specimen into at least two IRS-containing sub-specimens, a first one of which being designated as an addition-free IRS-containing sub-specimen; obtaining an addition-free mass spectrum of said addition-free IRS-containing sub-specimen; adding a known amount of said analyte (or a counterpart thereof) to at least one of the remaining of said IRS-containing sub-specimens to form at least one addition-present IRS-containing sub-specimen in which the concentration ratio of the analyte (or a counterpart thereof) to the IRS has been increased by a known amount; and then obtaining an addition-present mass spectrum of each of said addition-present IRS-containing sub-specimens; and using the ratio of the analyte signal (or the counterpart signal) to the IRS signal in said addition-free mass spectrum and each said addition-present mass spectrum to quantify said analyte.---;

---37. A method according to claim 36 in which said substep of using the ratio of the analyte signal (or a counterpart signal) to the IRS signal in said addition-free mass spectrum and each said addition-present mass spectrum to quantify said analyte comprises a substep of normalizing said addition-free mass spectrum and each said addition-present mass spectrum by dividing each mass spectrum by the respective IRS signals to determine the ratios of the analyte signals (or the counterpart signals) to the IRS signals for each mass spectrum.---;

---38. A method according to claim 36 in which said substep of obtaining an addition-present mass spectrum of an addition-present IRS-containing sub-specimen is repeated in a plurality of distinct, successive substeps to obtain a plurality of distinct, successive addition-present mass spectra of a plurality of distinct, successive addition-present sub-specimens of said IRS-containing specimen in which the concentration ratio of the analyte signal to the IRS signal is successively increased in known amounts.---;

---39. A method according to claim 38 in which said substep of adding a known amount of said analyte or a counterpart thereof to said IRS-containing specimen is repeated a plurality of successive times; whereby each repeated substep of adding a known amount of said analyte or a counterpart thereof precedes each of said distinct, successive substeps for obtaining each of said plurality of distinct, successive addition-present mass spectra.---;

---40. A method according to claim 33, in which said working curve analysis comprises substeps of:

a) obtaining a first mass spectrum of a first portion of said IRS-containing specimen; then,

b) making a plurality of standard preparations each containing a known but differing amount of said analyte or a counterpart thereof and each containing a known or equal

amount of said IRS; then, obtaining respective mass spectra of each of said plurality of standard preparations; whereby said respective mass spectra of said plurality of said standard preparations provide a working curve relationship of mass spectra relative to analyte concentration; and then,

c) using said first mass spectrum and the standard preparation mass spectra working curve relationship to quantify said analyte.---;

---41. A method according to claim 40 in which said substep of using said first mass spectrum and the standard preparation mass spectra working curve relationship to quantify said analyte comprises a substep of normalizing said first and each said standard preparation mass spectra by dividing each mass spectrum by the respective IRS signals to determine ratios of analyte signal to IRS signal for each mass spectrum.---;

---42. A method according to claim 34, in which said working curve analysis comprises substeps of:

a) obtaining a first mass spectrum of a first portion of said IRS-containing specimen; then,

b) making a single standard preparation containing a known amount of said analyte or a counterpart thereof and containing a known amount of said IRS which is known relative to the IRS concentration in said IRS-containing specimen; then, obtaining a mass spectrum of said standard preparation; whereby said mass spectrum of said standard preparation provides a single point working curve relationship of mass spectra relative to analyte concentration; and then,

c) using said first mass spectrum and the standard preparation mass spectrum single point working curve relationship to quantify said analyte.---;

---43. A method according to claim 42 in which said substep of using said first mass spectrum and the standard preparation mass spectrum single point working curve relationship to quantify said analyte comprises a substep of normalizing said first and said standard preparation mass spectrum by dividing each mass spectrum by the respective IRS signals to determine the ratios of analyte signal to IRS signal for each mass spectrum.---;

---44. A method according to claim 35 which involves said working curve analysis using multiple internal reference species, whereby:

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a) said step for ensuring that said specimen contains an IRS further comprises ensuring that said specimen contains a plurality of distinguishable internal reference species each in known and distinct concentrations; and

b) said step for capturing and isolating said analyte and said internal reference species using an affinity reagent further comprises capturing and isolating each of said plurality of internal reference species using an affinity reagent; and

c) said step for quantifying said analyte using mass spectrometric analysis further comprises: obtaining a mass spectrum of said IRS-containing specimen; whereby said respective mass spectra of said plurality of said internal reference species provide an analyte mass spectrum and a working curve relationship of mass spectra relative to analyte concentration; and then, using said analyte mass spectrum and the internal reference species working curve relationship to quantify said analyte.---;

---45. A method according to claim 44 in which said step for quantifying said analyte further comprises a substep of interpolating or extrapolating the analyte mass spectral signal magnitude relative to at least two internal reference species mass spectral signal